

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 04:37:24 ; Search time 1703.81 Seconds
(without alignments)
7460.491 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
c	1	364.8	69.8	558	9	AI503976	AI503976 vm43d08.x
c	2	363	69.4	623	9	AW146128	AW146128 um37e10.x
c	3	348.2	66.6	549	9	AI169253	AI169253 EST215088
c	4	347	66.3	558	9	AI265629	AI265629 uj04b07.x
	5	339.6	64.9	614	14	CD373004	CD373004 UI-R-GR0-
	6	339.2	64.9	816	9	AI119218	AI119218 ue94h02.y
	7	334.8	64.0	594	10	BF383724	BF383724 602044632
	8	334.4	63.9	796	14	CB959991	CB959991 AGENCOURT
c	9	322.2	61.6	499	9	AW495481	AW495481 UI-M-BH3-
c	10	320.8	61.3	642	9	AI876493	AI876493 uj59b10.x
c	11	320.8	61.3	673	12	BM984670	BM984670 UI-CF-EC1
c	12	316.8	60.6	575	9	AI248089	AI248089 qh69f05.x
c	13	309.2	59.1	468	9	AI169770	AI169770 EST215669
c	14	305	58.3	498	9	AA542914	AA542914 ni98c10.s
	15	299	57.2	882	9	AI604642	AI604642 vm43d08.y
c	16	296.4	56.7	653	13	BQ200567	BQ200567 UI-R-DZ1-
c	17	291.6	55.8	527	9	AA913900	AA913900 ol35g05.s
c	18	271.6	51.9	521	9	AW493459	AW493459 UI-M-BH3-
	19	271.6	51.9	559	12	BI715603	BI715603 ic34h10.y
	20	271.6	51.9	602	13	BU590710	BU590710 AGENCOURT
	21	271.6	51.9	621	12	BI221656	BI221656 602936980
	22	271.6	51.9	1658	11	AK081019	AK081019 Mus muscu
c	23	270.6	51.7	595	9	AI573421	AI573421 mo04b11.x
c	24	270	51.6	499	12	BI676839	BI676839 ic56a08.x
c	25	266.8	51.0	500	9	AA945553	AA945553 EST201052
c	26	266.8	51.0	525	9	AA963258	AA963258 UI-R-E1-g
	27	266	50.9	665	9	AA690767	AA690767 vu57d12.r
	28	265.2	50.7	559	12	BI715465	BI715465 ic33b09.y
	29	263.8	50.4	799	9	AI314558	AI314558 uj48d07.y
c	30	263.6	50.4	525	9	AI599751	AI599751 EST251454
c	31	261.4	50.0	499	12	BI294072	BI294072 UI-R-DK0-
c	32	260.4	49.8	561	12	BI714874	BI714874 ic33b09.x
c	33	258.4	49.4	502	9	AI104669	AI104669 EST213958
c	34	258	49.3	564	12	BI714981	BI714981 ic34h10.x
	35	256	48.9	2170	11	AK038119	AK038119 Mus muscu
c	36	254.8	48.7	430	9	AI478804	AI478804 tm52e04.x
	37	254.8	48.7	558	12	BI715475	BI715475 ic33c08.y
	38	250.8	48.0	512	9	AI876203	AI876203 uj59b10.y
	39	249.6	47.7	949	14	CB589117	CB589117 AGENCOURT
c	40	248.2	47.5	637	9	AW413016	AW413016 uq49h08.x
	41	246.4	47.1	473	9	AA451360	AA451360 vf84g03.r
c	42	246.4	47.1	486	9	AA993659	AA993659 ot85g11.s
	43	246.2	47.1	773	12	BI144500	BI144500 602908689
	44	243.2	46.5	482	9	AA456717	AA456717 aa13h06.r
c	45	243	46.5	474	9	AI526955	AI526955 uj48d07.x

ALIGNMENTS

RESULT 1

AI503976/c

LOCUS AI503976 558 bp mRNA linear EST 11-MAR-1999

DEFINITION vm43d08.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1001007 3' similar to gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI503976

VERSION AI503976.1 GI:4401827

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 558)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:565223

This clone was previously sequenced on the 5' end only, this new data is from the 3' end

High quality sequence stop: 440.

FEATURES

source

Location/Qualifiers

1. .558

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:1001007"

/tissue_type="diaphragm"

/dev_stage="adult"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="Stratagene mouse diaphragm (#937303)"

/note="Organ: diaphragm; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

BASE COUNT 103 a 133 c 149 g 173 t
ORIGIN

,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished
COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1006958
Seq primer: custom primer used
High quality sequence stop: 499.

FEATURES Location/Qualifiers
source 1. .623
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2247498"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
/clone_lib="Sugano mouse embryo mewa"
/note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAAGCTGCG and 3' end primer
CGACCTGCAGCTCGAGCACA."

BASE COUNT 123 a 138 c 170 g 191 t 1 others
ORIGIN

Query Match 69.4%; Score 363; DB 9; Length 623;
Best Local Similarity 81.9%; Pred. No. 2.5e-80;
Matches 433; Conservative 0; Mismatches 90; Indels 6; Gaps 1;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
||||| ||||| || | ||| |||||||||||||||||||||||||||||
Db 541 GGACCAGAGACCCTTTTCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 482

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
||||||||| ||||||||||| ||| ||||||||| |||||||||||
Db 481 AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTCGGAGGGGCACCTCAG 422

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
||||||| ||||||||| ||||||||| ||||||||| ||||| |||||
Db 421 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAATGTAC 362

Qy		181 TGTGCACCCCTCAAGCCGGCAAAGGCGAGCCCCTCCGTCCGTGCCAGCGCCACACCAC	240
Db		361 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCCTATCCGTGCCAGCGCCACACTGAC	302
Qy		241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAATGAAGTCTCAGAGG	300
Db		301 ATGCCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAACGAAGCTGCAAAGG	242
Qy		301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTG CAGGAAACAAGAACTA	360
Db		241 AGAAGGAAAGGAAGTACATTTGAAGAACCCAAGTAGAGGAAGTG CAGGAAACAAGACCTA	182
Qy		361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db		181 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG	122
Qy		421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTTGATC	474
Db		121 CTGCTTGAGCAACCTGCAAAACATCGAAACCCCTACCAAATAACAATAATAAGTCCAATA	62
Qy		475 ACATTTTC AAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC	523
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/mol_type="mRNA"
/db_xref="taxon:10118"
/clone="RKIBP33"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"

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BASE COUNT      112 a      140 c      133 g      164 t
ORIGIN

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Query Match          66.6%;  Score 348.2;  DB 9;  Length 549;
Best Local Similarity 81.8%;  Pred. No. 1.3e-76;
Matches 428;  Conservative 0;  Mismatches 88;  Indels 7;  Gaps 2;

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Qy      8 AGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCT 67
      |||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      549 AGACCCCTTTCGCGGGGCTGAGCTGGTGGACGCTCTTCAATTCGTGTGTGGACCAAGGGGCT 490

Qy      68 TTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCA 127
      |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      489 TTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTCTGAAGGGCACCACAGACGGGCA 430

Qy      128 TCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCAC 187
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Db      429 TTGTGGATGAGTGTAGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCTC 370

Qy      188 CCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGACATGCCCCA 247
      | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      369 CGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACATTGACATGCCCCA 310

Qy      248 AGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGA 307
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      309 AGACTCAGAAGTCCCAGCCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGGA 250

Qy      308 AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATG 367
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Db      249 AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACTTACAGAATG 190

Qy      368 TAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCA 427
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Db      129 AGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTTT 70

Qy      482 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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Db      69 AGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 27

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RESULT 4

AI265629/c

LOCUS AI265629 558 bp mRNA linear EST 18-NOV-1998

DEFINITION uj04b07.x1 Sugano mouse liver mlia Mus musculus cDNA clone

IMAGE:1890901 3' similar to gb:X04482 Mouse mRNA for
preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI265629

VERSION AI265629.1 GI:3883787
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 558)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HHMI Mouse EST Project
 JOURNAL Unpublished
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:975225
 Seq primer: custom primer used
 High quality sequence stop: 495.
 FEATURES Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1890901"
 /sex="female"
 /dev_stage="adult"
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 /clone_lib="Sugano mouse liver mlia"
 /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
 (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
 primer CGACCTGCAGCTCGAGCACA."
 BASE COUNT 106 a 135 c 156 g 161 t
 ORIGIN

Query Match 66.3%; Score 347; DB 9; Length 558;
 Best Local Similarity 82.0%; Pred. No. 2.5e-76;
 Matches 414; Conservative 0; Mismatches 85; Indels 6; Gaps 1;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	506	GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG	447
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	446	AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCTCAG	387
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	386	ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC	327
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240
Db	326	TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCAGCGCCACACTGAC	267
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	266	ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG	207
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	206	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA	147
Qy	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	146	CAGAATGTAGGAGGAGCCTCCACAGGAGCAGAAAATGCCACATCACC GCAGGATCCTTTG	87
Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC	474
Db	86	CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA	27
Qy	475	ACATTTCAAAGATGGCATTTCCTCC 499	
Db	26	ACATTACAAAGATGGGCATTTCCTCC 2	

COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: James Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/rat.html>
 Seq primer: M13 REVERSE.

FEATURES Location/Qualifiers
 source 1. .614
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-GR0-csv-j-17-0-UI"
 /tissue_type="Whole embryo"
 /dev_stage="embryo 13dpc"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-R-GR0"
 /note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
 UI-R-GR0 is a cDNA library containing the following
 tissue(s): rat whole embryo 13dpc. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. Denatured RNA was size
 fractionated on a 1% agarose gel. First strand cDNA
 synthesis was primed with oligo-dT primer containing a Not
 I site. Double strand cDNA was size selected according to
 mRNA size fraction, ligated with EcoR I adaptor, digested
 with NotI and then cloned directionally into pYX-Asc
 vector. The library tag sequence located between the Not I
 site and the polyA tail is CATCTCTACT. This library was
 created for the University of Iowa Program for Rat Gene
 Discovery and Mapping (Val Sheffield, Bento Soares and Tom
 Casavant)."

BASE COUNT 171 a 168 c 154 g 119 t 2 others
 ORIGIN

Query Match 64.9%; Score 339.6; DB 14; Length 614;
 Best Local Similarity 81.4%; Pred. No. 1.9e-74;
 Matches 393; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Qy 61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
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 Db 176 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGGCACACAG 235

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db 236 ACGGGCATTGTGGATGAGTGTTCCTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 295

Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db 296 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCATCCGGGCCCAGCGCCACACTGAC 355

Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db 356 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 415

Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db 416 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 475

Qy 361 CAGGATGTAGGAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCTTTG 420
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Db 476 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATTCCACGTACCGCATGATCCTTTG 535

Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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Db 536 CTGCTTGAGCAACCTGCANAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 595

Qy 481 CAA 483
 ||

Db 596 CCA 598

RESULT 6
 AI119218

LOCUS AI119218 816 bp mRNA linear EST 02-SEP-1998

DEFINITION ue94h02.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:1498803 5' similar to gb:X04482 Mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI119218

VERSION AI119218.1 GI:3519542

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 816)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE The WashU-HHMI Mouse EST Project

JOURNAL Unpublished

COMMENT Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: custom primer used
High quality sequence stop: 473.

BASE COUNT	230 a	219 c	172 g	187 t	8 others
ORIGIN					

Query Match 64.9%; Score 339.2; DB 9; Length 816;
Best Local Similarity 81.2%; Pred. No. 2.5e-74;
Matches 389; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

[illegible]

Qy 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
 ||| ||||| || || ||| | |||| | | || | ||||| || |||||
 Db 683 CAGAATGTANGAGGAGCCTNCCACGGAGCAGAANATGCCACATCACCGCANGATCCTTTG 742

Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATT 479
 || | |||| | || ||| ||||| || | | | | || |
 Db 743 CTGCTTGAGCAACCTGCANAACATCGAAACACCTACCAAATAACATNTATAAGTCCAAT 801

RESULT 7

BF383724

LOCUS BF383724 594 bp mRNA linear EST 27-NOV-2000

DEFINITION 602044632F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4194295 5', mRNA sequence.

ACCESSION BF383724

VERSION BF383724.1 GI:11365029

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 594)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9527 row: p column: 08

High quality sequence stop: 589.

FEATURES Location/Qualifiers

source

1. .594

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4194295"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_Li9"

/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 175 a 162 c 142 g 115 t

ORIGIN

Query Match 64.0%; Score 334.8; DB 10; Length 594;

Best Local Similarity 82.0%; Pred. No. 2.9e-73;

Matches 400; Conservative 0; Mismatches 82; Indels 6; Gaps 1;

Qy 16 TGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTTC 75

cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDAM371 row: p column: 18

High quality sequence stop: 707.

FEATURES
source Location/Qualifiers
1. .796
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30341081"
/tissue_type="Human Placenta"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
allI-XhoI; Site_2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

BASE COUNT 224 a 197 c 191 g 184 t
ORIGIN

Query Match 63.9%; Score 334.4; DB 14; Length 796;
Best Local Similarity 84.6%; Pred. No. 3.9e-73;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
|||||
Db 180 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 239
Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
|||||
Db 240 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 299
Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
|||||
Db 300 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 359
Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
|| |||||
Db 360 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 419
Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
|||||
Db 420 ATGCCCAAGACCCAG----- 434
Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
|||||
Db 435 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 487
Qy 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420


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/clone="UI-M-BH3-auy-g-11-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_M_S4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=NIH_BMAP_M_S4
TAG_TISSUE=pineal-glands
TAG_SEQ=CAGAC"

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BASE COUNT      86 a      112 c      124 g      177 t
ORIGIN

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Query Match          61.6%; Score 322.2; DB 9; Length 499;
Best Local Similarity 82.3%; Pred. No. 4e-70;
Matches 396; Conservative 0; Mismatches 78; Indels 7; Gaps 2;

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Qy      50 TGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGA 109
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      499 TGTGTGGACCGAGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTGGA 440

Qy      110 GGGCACCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGC 169
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      439 GGGCACCTCAGACAGGCATTGTGGATGAGTGCTTCCGGAGCTGTGATCTGAGGAGAC 380

Qy      170 TGGAGATGTACTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGC 229
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      379 TGGAGATGTACTGTGCCCCACTGAAGCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGC 320

Qy      230 GCCACACCGACATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGA 289
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      319 GCCCACTGACATGCCCAAGACTCAGAAGTCCCGTCCCTATCGACAAACAAGAAAACGA 260

Qy      290 AGTCTCAGAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGA 349

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      ||  || |||||
Db      259 AGCTGCAAAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGA 200

Qy      350 AACAGAAGTACAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGC 409
      ||||| ||||| ||||| || ||| | ||| | ||| |||||
Db      199 AACAGACCTACAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGC 140

Qy      410 AGGACCCCTTTGCTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAA 463
      |||| ||||| ||||| | ||||| || ||| || || ||
Db      139 AGGATCCTTTGCTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAA 80

Qy      464 TAAGTTTGATCACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT 522
      |||| | ||||| ||||| ||||| ||||| ||||| |||||
Db      79 TAAGTCCAATAACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATT 20

Qy      523 C 523
      |
Db      19 C 19

```

RESULT 10

AI876493/c

LOCUS AI876493 642 bp mRNA linear EST 21-JUL-1999

DEFINITION uj59b10.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1924219 3' similar to gb:X57025_rnal INSULIN-LIKE GROWTH
FACTOR IA PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for
preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI876493

VERSION AI876493.1 GI:5550542

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 642)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:980511

Seq primer: custom primer used

High quality sequence stop: 257.

FEATURES

source

Location/Qualifiers

1. .642

/organism="Mus musculus"

/mol_type="mRNA"

```

/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1924219"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."

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BASE COUNT      127 a      154 c      175 g      185 t      1 others
ORIGIN

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Query Match          61.3%; Score 320.8; DB 9; Length 642;
Best Local Similarity 80.1%; Pred. No. 9.6e-70;
Matches 403; Conservative 0; Mismatches 93; Indels 7; Gaps 2;

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```

Qy      2  GACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACA 61
      |||| |||| || |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      503 GACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGGTCGTGTGTGGACCGA 444

Qy      62  GGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGA 121
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      443 GGGGCTTTTCTTCAACAAGCCACAGGCTATGGCTCCAGCATTTGGAGGGCACCTCAGA 384

Qy      122 CAGGCATCGTGGATGAGTGCTGCTTCCGG-AGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      ||| || |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      383 CAGTCAATGTGGATGAGTGTTGCTTCCGGAAGCTGTGATCTGAGAAGACTGNAGATGTAC 324

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||| || || |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      323 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCAGCGCCACACTGAC 264

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      263 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 204

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      203 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 144

Qy      361 CAGGATGTAGGAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCTTTTG 420
      ||| |||| |||| || |||| |||| || || || || |||| |||| |||| ||||
Db      143 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTTG 84

Qy      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
      ||      |      |||| | || || || ||      || |||| || ||

```

Db 83 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 24

Qy 475 ACATTTCAAAGATGGCATTTCCT 497

||||| ||||| || ||

Db 23 ACATTACAAAGATGGGCATTTC 1

RESULT 11

BM984670/c

LOCUS BM984670 673 bp mRNA linear EST 20-FEB-2003

DEFINITION UI-CF-EC1-abj-k-24-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-abj-k-24-0-UI 3', mRNA sequence.

ACCESSION BM984670

VERSION BM984670.1 GI:19610417

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 673)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1. .673

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-CF-EC1-abj-k-24-0-UI"

/tissue_type="Lung"

/dev_stage="Adult and Fetal"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-CF-EC1"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was

constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.

TAG_LIB=UI-CF-EC1

TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383

TAG_SEQ=AAGTGCTTAC"

BASE COUNT 152 a 164 c 169 g 188 t

ORIGIN

Query Match 61.3%; Score 320.8; DB 12; Length 673;
Best Local Similarity 84.2%; Pred. No. 9.7e-70;
Matches 443; Conservative 0; Mismatches 27; Indels 56; Gaps 5;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||||||||||||||| ||||||||||||||||||||||||||||||||
Db     492 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 433

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      ||||| ||||||||| ||||||||| || ||||||||||||||||||| |||||
Db     432 AGGGG-TTTTATTTCAAGCAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 374

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     373 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 314

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      || |||||||||||| || ||| |||| ||||| |||||||||||||||||
Db     313 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 254

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      ||||||||| |||
Db     253 ATGCCCAAGACCCAG----- 239

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||||||||||||||| |||||||||||||||||||||||||||||
Db     238 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 186

Qy     361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||||||||||||||| |||||||||||| |||| |||||||||||| |||||
Db     185 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 126

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      ||||||| |||||||| |||| ||||| ||| |||||||||||||||| ||||
Db     125 CTCTGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 66

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
      || ||||| ||| |||||||||||||||||||||||||
Db     65 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 20

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RESULT 12
 AI248089/c
 LOCUS AI248089 575 bp mRNA linear EST 01-DEC-1998
 DEFINITION qh69f05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
 clone IMAGE:1849953 3' similar to gb:X57025_rnal INSULIN-LIKE
 GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION AI248089
 VERSION AI248089.1 GI:3843486
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 575)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 918 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 380.
 FEATURES
 source Location/Qualifiers
 1. .575
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1849953"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
 with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
 This is a subtracted version of the original Soares fetal
 liver spleen 1NFLS library. 1st strand cDNA was primed
 with a Pac I - oligo(dT) primer [5'
 AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."
 BASE COUNT 135 a 152 c 131 g 156 t 1 others
 ORIGIN
 Query Match 60.6%; Score 316.8; DB 9; Length 575;
 Best Local Similarity 83.8%; Pred. No. 9.4e-69;
 Matches 428; Conservative 0; Mismatches 28; Indels 55; Gaps 4;
 Qy 16 TGC GGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTTC 75
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 Db 551 TGC GGGGCTGAGCTGGTGNATGCTCTTCAGTTCGTGTGTGAAGACAGGGGCTTTTATTTTC 492

Qy	76	AACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCATCGTGGAT	135
Db	491	AACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAGACAGGCATCGTGGAT	432
Qy	136	GAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCACCCCTCAAG	195
Db	431	GAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAG	372
Qy	196	CCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACTCAG	255
Db	371	CCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACCCAG	312
Qy	256	AAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGAAAGGAAGT	315
Db	311	-----AAGGAAGT	304
Qy	316	ACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA	375
Db	303	ACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA	244
Qy	376	CCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCAC-AGTTAC	434
Db	243	CCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTCTGCACGAGTTAC	184
Qy	435	CTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAAAGAT-GGCAT	492
Db	183	CTGTTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACATTTAAAAGATGGGCGT	124
Qy	493	TTCCCCCAATGAAATACACAAGTAAACATT	523
Db	123	TTCCCCCAATGAAATACACAAGTAAACATT	93

Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

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 /note="Organ: liver; Vector: pT7T3Pac; Site_1: EcoRI;
 Site_2: NotI"

BASE COUNT 85 a 115 c 119 g 149 t
ORIGIN

Query Match 59.1%; Score 309.2; DB 9; Length 468;
Best Local Similarity 81.8%; Pred. No. 7.2e-67;
Matches 383; Conservative 0; Mismatches 78; Indels 7; Gaps 2;

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Qy      63 GGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGAC 122
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Qy      123 AGGCATCGTGGATGAGTGTCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTG 182
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Db      408 GGGCATTGTGGATGAGTGTCTGCTCCCGAGCTGTGATCTGAGGAGGTTGGAGATGTACTG 349

Qy      183 TGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACAT 242
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Db      348 TGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACAT 289

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Qy      303 AAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACA 362
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Db      228 AAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACA 169

Qy      363 GGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCT 422
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Db      168 GAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCT 109

Qy      423 CTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATCAC 476
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Db      108 GCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACC 49

Qy      477 ATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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RESULT 14
AA542914/c
LOCUS

AA542914

498 bp

mRNA

linear

EST 19-AUG-1997


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                  (HUMAN);, mRNA sequence.
ACCESSION       AA542914
VERSION         AA542914.1  GI:2291394
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 498)
AUTHORS         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                  Tumor Gene Index
JOURNAL         Unpublished
COMMENT         Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-r@mail.nih.gov
                  Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
                  Emmert-Buck, M.D., Ph.D.
                  cDNA Library Preparation: M. Bento Soares, Ph.D.
                  cDNA Library Arrayed by: Greg Lennon, Ph.D.
                  DNA Sequencing by: Washington University Genome Sequencing Center
                  Clone distribution: NCI-CGAP clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  www-bio.llnl.gov/bbrp/image/image.html
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                  High quality sequence stop: 412.
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                     /clone="IMAGE:984882"
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                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Pr21"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; 1st strand cDNA was prepared
                     from normal prostate bulk tissue, and was then primed with
                     a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library is not normalized. Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        105 a    135 c    123 g    135 t
ORIGIN
Query Match              58.3%;  Score 305;  DB 9;  Length 498;
Best Local Similarity    83.5%;  Pred. No. 8.2e-66;
Matches 440;  Conservative 0;  Mismatches 30;  Indels 57;  Gaps 6;

Qy      1  GGACCGGAGACGCTCTGCGGTGC-TGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 59
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Db      476 GGACCGGAGAACTTTTGCGGGGCTTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 417

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Qy	60	CAGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCA	119
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Qy	120	GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTA	179
Db	357	GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTA	298
Qy	180	CTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGA	239
Db	297	TTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGA	238
Qy	240	CATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAG	299
Db	237	CATGCCCAAGACCCAG-----	222
Qy	300	GAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACT	359
Db	221	-----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACT	170
Qy	360	ACAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTT	419
Db	169	ACAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTT	110
Qy	420	GCTCTGCAC--AGTTACCTG--TAAACATTGGAATACCGCCAAAAAATAAGTTTGATCACA	477
Db	109	GCTCTGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACA	50
Qy	478	TTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC	523
Db	49	TTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC	3

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:565223
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 361.

FEATURES	Location/Qualifiers
source	1. .882
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	/tissue_type="diaphragm"
	/dev_stage="adult"
	/lab_host="SOLR (kanamycin resistant)"
	/clone_lib="Stratagene mouse diaphragm (#937303)"
	/note="Organ: diaphragm; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA, prepared from diaphragm muscle. Primer: Oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

BASE COUNT 236 a 226 c 183 g 223 t 14 others
 ORIGIN

Query Match 57.2%; Score 299; DB 9; Length 882;
 Best Local Similarity 77.2%; Pred. No. 3e-64;
 Matches 393; Conservative 0; Mismatches 109; Indels 7; Gaps 3;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
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Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	437	AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTTCAGGGCACCTCAG	496
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	497	ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGANGAGACTGGAGATGTAC	556
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Db	557	TGTGCCCCACTGAAGCCTACANAAGCAGCCGCTCTATCCGTGCCCAGCGCCACACTGAC	616
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	617	ATGCNNCAGACTCAGAAGTCCCCGTNCCTATCGACNNAACAGAAAACGAAGCTTGCAAGG	676
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTA	360

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Db      677 GAGAGGGAAGGGAGTACATTTGAGGAACACANGTNGAGGAAGTGCANGAAACAAGACCTA 736
Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db      737 CCAGATGTANGAGGAGCCTTC--AACCGAGCAGAAATGCACATCACCCGNAGATCCTTTG 794
Qy      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAA----AAAATAAGTTTGATCAC 476
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Db      795 CT-GCTTGAGCTAACTGCAAACATCGAACCACCTTACCAATTACAATAATAAGTTCAATAA 853
Qy      477 ATTTCAAAGATGGCATTTCCTCCCAATGAA 505
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Db      854 CATACAAAGATGGCATTTCCTCCCAATGAA 882

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Search completed: December 13, 2003, 07:29:51
Job time : 1704.81 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 05:41:20 ; Search time 2336.77 Seconds
(without alignments)
9156.102 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
1	523	100.0	523	6	AX147746	AX147746 Sequence
2	523	100.0	523	6	AX300783	AX300783 Sequence
3	467.4	89.4	517	6	AX147742	AX147742 Sequence
4	467.4	89.4	517	6	AX300779	AX300779 Sequence
5	409	78.2	471	6	AX147754	AX147754 Sequence
6	409	78.2	471	6	AX300791	AX300791 Sequence
7	364.8	69.8	1536	10	BC012409	BC012409 Mus muscu
8	361.6	69.1	798	10	RNIGFI2	X06108 Rat mRNA (c
9	361.6	69.1	958	10	RNIGFI1	X06107 Rat mRNA (c
10	358.4	68.5	710	10	RATIGFIA	M15480 Rat insulin
11	356.8	68.2	539	6	AX147744	AX147744 Sequence
12	356.8	68.2	539	6	AX300781	AX300781 Sequence
13	349.4	66.8	651	10	MMIGFIBR	X04482 Mouse mRNA
14	336	64.2	432	4	AF022961	AF022961 Oryctolag
15	334.4	63.9	7260	6	AX375028	AX375028 Sequence
16	334.4	63.9	7260	6	AX411095	AX411095 Sequence
17	334.4	63.9	7260	9	HSIGFACI	X57025 Human IGF-I
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19	332.8	63.6	725	9	HSIGFI	X00173 Homo sapien
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21	332.4	63.6	616	9	HSIGF1A	X56773 H.sapiens m
22	331.2	63.3	620	6	I08370	I08370 Sequence 2
23	331.2	63.3	1076	9	HUMIGFI	M27544 Human insul
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25	293.8	56.2	532	4	SSILGF1M	X17492 Porcine mRN
26	293.8	56.2	567	4	PIGGFIIA	M31175 Pig insulin
27	286.2	54.7	888	4	ECU85272	U85272 Equus cabal
28	281.8	53.9	978	4	GOTIGFI	D11378 Goat mRNA f
29	281.8	53.9	978	6	E05279	E05279 DNA encodin
30	280.2	53.6	1284	4	BTILGF1A	X15726 Bovine mRNA
31	275.4	52.7	747	4	SHPIGFIA6	M31735 Sheep insul
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33	275.4	52.7	1015	4	SHPIGFIA46	M31736 Sheep insul

34	275.4	52.7	1107	4	SHPIGF1A1	M30653 Sheep insul
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36	275.2	52.6	1094	9	HUMGF1B	M11568 Human insul
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39	274.6	52.5	3599	6	BD063790	BD063790 Insulin-1
40	274.6	52.5	3599	6	BD069041	BD069041 Treatment
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42	274.6	52.5	3600	6	BD069040	BD069040 Treatment
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44	271.6	51.9	696	10	MMIGFIAR	X04480 Mouse mRNA
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ALIGNMENTS

RESULT 1

AX147746

LOCUS AX147746 523 bp DNA linear PAT 31-AUG-2001

DEFINITION Sequence 5 from Patent WO0136483.

ACCESSION AX147746

VERSION AX147746.1 GI:14346791

KEYWORDS .

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink, G.R. and Johnson, I.R.

TITLE Use of the insulin-like-growth factor i isoform mgf for the
treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 5 25-MAY-2001;

University College London (GB)

FEATURES Location/Qualifiers

source

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/db_xref="taxon:9986"

CDS

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BASE COUNT 154 a 129 c 142 g 98 t

ORIGIN

Query Match 100.0%; Score 523; DB 6; Length 523;

Best Local Similarity 100.0%; Pred. No. 9.5e-150;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Qy          121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db          301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Qy          361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db          361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db          421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT 480
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Db          481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523

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RESULT 2

AX300783

LOCUS AX300783 523 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 5 from Patent WO0185781.

ACCESSION AX300783

VERSION AX300783.1 GI:17382064

KEYWORDS .

SOURCE *Oryctolagus cuniculus* (rabbit)

ORGANISM *Oryctolagus cuniculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; *Oryctolagus*.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 5 15-NOV-2001;

University College London (GB) ; East Grinstead Medical Research
Trust (GB)

FEATURES

source

Location/Qualifiers

1. .523

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/mol_type="genomic DNA"

/db_xref="taxon:9986"

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 BASE COUNT 154 a 129 c 142 g 98 t
 ORIGIN

Query Match 100.0%; Score 523; DB 6; Length 523;
 Best Local Similarity 100.0%; Pred. No. 9.5e-150;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Db	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Qy	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	480
Db	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	480
Qy	481	CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC	523
Db	481	CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC	523

RESULT 3
 AX147742
 LOCUS AX147742 517 bp DNA linear PAT 31-AUG-2001
 DEFINITION Sequence 1 from Patent WO0136483.
 ACCESSION AX147742

VERSION AX147742.1 GI:14346787
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Goldspink, G.R. and Johnson, I.R.
 TITLE Use of the insulin-like-growth factor i isoform mgf for the
 treatment of neurological disorders
 JOURNAL Patent: WO 0136483-A 1 25-MAY-2001;
 University College London (GB)
 FEATURES Location/Qualifiers
 source 1..517
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 CDS <1..333
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC41175.1"
 /db_xref="GI:14346788"
 /db_xref="REMTREMBL:CAC41175"
 /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSSRRAPQTGIV
 DECCFRSCDLRRLEMYCAPLKPASARSVRAQRHTDMPKTQKYQPPSTNKNTKSQRRK
 GSTFEEHK"
 BASE COUNT 150 a 130 c 139 g 98 t
 ORIGIN

Query Match 89.4%; Score 467.4; DB 6; Length 517;
 Best Local Similarity 96.2%; Pred. No. 1.3e-132;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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 Db 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
 |||||
 Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 |||||
 Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
 |||||
 Db 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
 Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 |||||
 Db 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||||
 Db 298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
 |||||
 Db 358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
 |||||
 Db 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
 Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521
 |||||
 Db 477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517

RESULT 4

AX300779

LOCUS AX300779 517 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 1 from Patent WO0185781.

ACCESSION AX300779

VERSION AX300779.1 GI:17382060

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 1 15-NOV-2001;
 University College London (GB) ; East Grinstead Medical Research
 Trust (GB)

FEATURES

source

Location/Qualifiers

1. .517

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

CDS

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/note="unnamed protein product"

/codon_start=1

/protein_id="CAD13040.1"

/db_xref="GI:17382061"

/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRAPQTGIV
 DECCFRSCDLRRLEMYCAPLKPASARSVRAQRHTDMPKTQKYQPPSTNKNTKSQRRK
 GSTFEEHK"

BASE COUNT 150 a 130 c 139 g 98 t

ORIGIN

Query Match 89.4%; Score 467.4; DB 6; Length 517;

Best Local Similarity 96.2%; Pred. No. 1.3e-132;

Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60
 |||||
 Db 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60
 Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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 Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 |||
 Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 |||
 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
 || |||
 Db 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
 |||
 Qy 241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 |||
 Db 241 ATGCCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA--G 297
 |||
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||
 Db 298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
 |||
 Qy 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
 |||
 Db 358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
 |||
 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
 |||
 Db 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
 |||
 Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521
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 Db 477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
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RESULT 5

AX147754

LOCUS AX147754 471 bp DNA linear PAT 08-JUN-2001

DEFINITION Sequence 13 from Patent WO0136483.

ACCESSION AX147754

VERSION AX147754.1 GI:14348552

KEYWORDS .

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink,G.R. and Johnson,I.R.

TITLE Use of the insulin-like-growth factor i isoform mgf for the
 treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 13 25-MAY-2001;
 University College London (GB)

FEATURES

Location/Qualifiers

source

1. .471

/organism="Oryctolagus cuniculus"

/mol_type="genomic DNA"

/db_xref="taxon:9986"

CDS

<1. .318

/note="unnamed protein product"

/codon_start=1

/protein_id="CAC41264.1"

/db_xref="GI:14348553"

/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSSRRAPQTGIV
DECCFRSCDLRRLLEMYCAPLKPAKAARSVRAQRHTDMPKTQKEVHLKNTSRGSAGNKN
YRM"

BASE COUNT 132 a 118 c 131 g 90 t
ORIGIN

Query Match 78.2%; Score 409; DB 6; Length 471;
Best Local Similarity 90.1%; Pred. No. 1.3e-114;
Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

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Qy      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61  AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
          |||
Db     61  AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||
Db    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
          |||
Db    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241  ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||
Db    241  ATGCCCCAAGACTCAG----- 255

Qy    301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          |||
Db    256  -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy    361  CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
          |||
Db    309  CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy    421  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
          |||
Db    369  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy    481  CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
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Db    429  CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 471
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RESULT 6

AX300791

LOCUS AX300791 471 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 13 from Patent WO0185781.

ACCESSION AX300791

VERSION AX300791.1 GI:17382072

KEYWORDS .

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink,G.D. and Terenghi,G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 13 15-NOV-2001;
University College London (GB) ; East Grinstead Medical Research
Trust (GB)

FEATURES Location/Qualifiers

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/organism="Oryctolagus cuniculus"
/mol_type="genomic DNA"
/db_xref="taxon:9986"

CDS <1. .318
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD13045.1"
/db_xref="GI:17382073"
/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRAPQTGIV
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YRM"

BASE COUNT 132 a 118 c 131 g 90 t

ORIGIN

Query Match 78.2%; Score 409; DB 6; Length 471;
Best Local Similarity 90.1%; Pred. No. 1.3e-114;
Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240
Db	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	241	ATGCCCAAGACTCAG-----	255
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	256	-----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	308
Qy	361	CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	309	CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	368
Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	480

Db 369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
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Db 429 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 471

RESULT 7

BC012409

LOCUS BC012409 1536 bp mRNA linear ROD 16-APR-2003

DEFINITION Mus musculus insulin-like growth factor 1, mRNA (cDNA clone MGC:18617 IMAGE:4194295), complete cds.

ACCESSION BC012409

VERSION BC012409.1 GI:15214568

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1536)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1536)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 24 Row: k Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6754307.

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FEATURES             Location/Qualifiers
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                        /mol_type="mRNA"
                        /strain="FVB/N"
                        /db_xref="taxon:10090"
                        /clone="MGC:18617 IMAGE:4194295"
                        /tissue_type="Liver, normal. 5 month old male mouse."
                        /clone_lib="NCI_CGAP_Li9"
                        /lab_host="DH10B"
    gene               1. .1536
                        /gene="Igfl"
                        /db_xref="LocusID:16000"
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    CDS                28. .429
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                        /db_xref="GI:15214569"
                        /db_xref="LocusID:16000"
                        /translation="MSSSHLFYLAALCLLTFTSSTTAGPETLCGAELVDALQFVCGPRG
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BASE COUNT 485 a 324 c 303 g 424 t
ORIGIN

Query Match 69.8%; Score 364.8; DB 10; Length 1536;
Best Local Similarity 83.2%; Pred. No. 6.6e-101;
Matches 441; Conservative 0; Mismatches 82; Indels 7; Gaps 2;

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Qy      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      94  GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 153

Qy      61  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db     154  AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTCCGAGGGCACCTCAG 213

Qy     121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db     214  ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 273

Qy     181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

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              /protein_id="CAA29481.1"
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BASE COUNT    238 a    196 c    183 g    181 t
ORIGIN

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Query Match          69.1%; Score 361.6; DB 10; Length 798;
Best Local Similarity 82.8%; Pred. No. 5.8e-100;
Matches 439; Conservative 0; Mismatches 84; Indels 7; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      217 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 276

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db      277 AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACACAG 336

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db      337 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 396

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
        ||||| || || ||||| ||||| ||||| || || || ||||| ||||| |||||
Db      397 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCATCCGGGCCAGCGCCACACTGAC 456

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        ||||| ||||| ||||| ||||| || || || ||||| ||||| || || ||
Db      457 ATGCCCAAGACTCAGAAGTCCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 516

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db      517 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 576

Qy      361 CAGGATGTAGGAAGACCC'TTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCC'TTG 420
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Db      577 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 636

Qy      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
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Db      637 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 696

Qy      475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
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Db      697 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 746

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RESULT 9
RNIGF11

Qy	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	532	CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG	591
Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC	474
Db	592	CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA	651
Qy	475	ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC	523
Db	652	CCATTTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC	701

Query Match 68.2%; Score 356.8; DB 6; Length 539;
Best Local Similarity 82.3%; Pred. No. 1.6e-98;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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KGSTLEEHK"

BASE COUNT 161 a 136 c 139 g 103 t
ORIGIN

Query Match 68.2%; Score 356.8; DB 6; Length 539;
Best Local Similarity 82.3%; Pred. No. 1.6e-98;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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Db      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCCGAGGGGCACCACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCATCCGGGCCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
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Qy    475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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RESULT 13

MMIGFIBR

LOCUS MMIGFIBR 651 bp mRNA linear ROD 21-MAR-1995
DEFINITION Mouse mRNA for preproinsulin-like growth factor IB.
ACCESSION X04482
VERSION X04482.1 GI:51806
KEYWORDS growth factor; insulin-like growth factor IB; preproinsulin-like

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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 Db 199 AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTCCGAGGGCACCTCAG 258
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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 Db 259 ACAGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318
 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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 Db 319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 378
 Qy 241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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 Db 379 ATGCCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||||
 Db 439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498
 Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
 |||||
 Db 499 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCAGGATCCTTTG 558
 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
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 Db 559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618
 Qy 475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 506
 |||||
 Db 619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651

RESULT 14

AF022961

LOCUS AF022961 432 bp mRNA linear MAM 14-OCT-1997

DEFINITION *Oryctolagus cuniculus* insulin-like growth factor IB (IGF-IB) mRNA, complete cds.

ACCESSION AF022961

VERSION AF022961.1 GI:2522201

KEYWORDS .

SOURCE *Oryctolagus cuniculus* (rabbit)

ORGANISM *Oryctolagus cuniculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; *Oryctolagus*.

REFERENCE 1 (bases 1 to 432)

AUTHORS Flekna,G., Brem,G. and Mueller,M.

TITLE Direct Submission

JOURNAL Submitted (05-SEP-1997) Institute of Animal Breeding and Genetics, Veterinary University of Vienna, Veterinaerplatz 1, Vienna A-1210, Austria

FEATURES

source Location/Qualifiers
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CDS       1. .432
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BASE COUNT      105 a      126 c      115 g      86 t
ORIGIN

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Query Match          64.2%; Score 336; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 4.1e-92;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     157 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 216

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db     217 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 276

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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RESULT 15
AX375028
LOCUS      AX375028              7260 bp      DNA      linear      PAT 01-MAR-2002
DEFINITION Sequence 31 from Patent WO0210436.
ACCESSION  AX375028
VERSION    AX375028.1  GI:19169860
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE      1
AUTHORS        Baak, J. and Mutter, G.L.
TITLE          Prognostic classification of breast cancer
JOURNAL        Patent: WO 0210436-A 31 07-FEB-2002;
               THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US)
FEATURES
  source        Location/Qualifiers
                1. .7260
                /organism="Homo sapiens"
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BASE COUNT     2330 a   1415 c   1240 g   2275 t
ORIGIN

Query Match          63.9%; Score 334.4; DB 6; Length 7260;
Best Local Similarity 84.6%; Pred. No. 2e-91;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db      551 ATGCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
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Db      619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
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Db      679 CTCTGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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Searched: 2552756 seqs, 1349719017 residues

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query						
No.	Score	Match	Length	DB	ID		
1	523	100.0	523	22	AAD06400		Rabbit IGF-I isofo
2	523	100.0	523	24	AAS16879		Rabbit mechano-gro
3	523	100.0	553	18	AAT84893		Rabbit insulin lik
4	467.4	89.4	517	22	AAD06398		Human IGF-I isofo
5	467.4	89.4	517	24	AAS16877		Human mechano-grow
6	409	78.2	471	22	AAD06405		Rabbit liver-type
7	409	78.2	471	24	AAS16884		Rabbit insulin-lik
8	356.8	68.2	539	22	AAD06399		Rat IGF-I isoform
9	356.8	68.2	539	24	AAS16878		Rat mechano-growth
10	349.4	66.8	651	25	ABV76185		Mouse insulin-like
11	334.4	63.9	818	8	AAN70436		Sequence encoding
12	334.4	63.9	7260	24	ABT11091		Human breast cance
13	334.4	63.9	7260	24	ABK84583		Human cDNA differe
14	334.4	63.9	7260	24	ABN97244		Gene #3742 used to
15	334.4	63.9	7260	24	ABK64812		Human benign prost
16	334.4	63.9	7260	24	ABK35504		Human endometrial
17	334.4	63.9	7260	24	ABK35561		Gene IGF1 differen
18	332.8	63.6	777	18	AAT84894		Human insulin like
19	331.2	63.3	622	7	AAN60490		Human prepro-somat
20	281.8	53.9	978	14	AAQ47804		Sequence encoding
21	275.2	52.6	1136	8	AAN70435		Sequence encoding
22	274.6	52.5	3599	19	AAV50428		Plasmid pIG0552 lo
23	274.6	52.5	3599	19	AAV40796		Actual sequence of
24	274.6	52.5	3600	19	AAV50427		Plasmid pIG0552 up
25	274.6	52.5	3600	19	AAV40795		Expected sequence
26	274.6	52.5	5707	20	AAX88055		Plasmid pIG0335 DN
27	274.6	52.5	6345	20	AAX88054		Plasmid pIG0100A D
28	273.6	52.3	612	22	AAS14695		Human cDNA encodin
29	273.6	52.3	612	25	ABZ83309		Toxicologically re
30	266.8	51.0	1052	20	AAX27498		Rat liver form of
31	262	50.1	487	22	AAD06404		Rat liver-type IGF
32	262	50.1	487	24	AAS16883		Rat insulin-like g
33	250	47.8	671	24	ABT09479		Phase-1 Rat CT gen
34	237.6	45.4	317	24	AAS16882		Human insulin-like
35	237.6	45.4	318	22	AAD06403		Human liver-type I
36	237.6	45.4	462	19	AAV50426		Human IGF-1 encodi
37	237.6	45.4	462	19	AAV40794		Human IGF-I coding
38	237.6	45.4	462	24	ABZ35734		Human IGF1 polynuc
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40	237.6	45.4	462	24	ABV78158		Human IGF1 DNA SEQ
41	237.6	45.4	462	24	ABL91699		Human polynucleoti
42	209	40.0	286	25	ABV76186		Mouse insulin-like
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44	193	36.9	210	24	AAD44955		Human insulin grow
45	193	36.9	210	24	ABA03146		Native mature IGF-

ALIGNMENTS

RESULT 1

AAD06400

ID AAD06400 standard; cDNA; 523 BP.

XX

AC AAD06400;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;

KW sex-linked muscular dystrophy; peripheral neuropathy;

KW Alzheimer's disease; Parkinson's disease; ss.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /*tag= a

FT /product= "Mechano-growth factor (MGF)"

FT /note= "This region comprises exons 3-6. The CDS does

FT not include start codon"

FT /partial

XX

PN WO200136483-A1.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-GB04354.

XX

PR 15-NOV-1999; 99GB-0026968.

XX

PA (UNLO) UNIV COLLEGE LONDON.

XX

PI Goldspink G, Johnson I;

XX

DR WPI; 2001-355620/37.

DR P-PSDB; AAE02449.

XX

PT Use of mechano-growth factor, an isoform of Insulin-like Growth

PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a

PT medicament for the treatment of neurological disorder -

XX

PS Claim 4; Page 53-54; 66pp; English.

XX

CC The present invention relates to use of mechano-growth factor (MGF),

CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a

CC medicament for the treatment of neurological disorder. The MGF is capable

CC of reducing motoneurone loss by 20% or greater in response to nerve

CC avulsion, and effects motoneurone rescue, preferably adult motoneurone

CC rescue. The MGF polynucleotide and polypeptide are useful in the

CC manufacture of a medicament for the treatment of a neurological disorder,

CC including a disorder of motoneurons and/or neurodegenerative disorder,

CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (Ec) domain, hence also referred as
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.

XX

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 100.0%; Score 523; DB 22; Length 523;
 Best Local Similarity 100.0%; Pred. No. 5.1e-144;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Db	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTA	360
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Qy	361	CAGGATGTAGGAAGACCC'TTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	361	CAGGATGTAGGAAGACCC'TTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	480
Db	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	480
Qy	481	CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC	523
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RESULT 2

AAS16879
ID AAS16879 standard; cDNA; 523 BP.
XX
AC AAS16879;
XX
DT 25-FEB-2002 (first entry)
XX
DE Rabbit mechano-growth factor (MGF) cDNA.
XX
KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
KW nerve avulsion.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..336
FT /*tag= a
FT /product= "Rabbit MGF"
FT /partial
FT /note= "No start codon"
FT exon 1..76
FT /*tag= b
FT /number= 3
FT exon 77..259
FT /*tag= c
FT /number= 4
FT exon 260..309
FT /*tag= d
FT /number= 5
FT exon 311..333
FT /*tag= e
FT /number= 6
XX
PN WO200185781-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-GB02054.
XX
PR 10-MAY-2000; 2000GB-0011278.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI Goldspink G, Terenghi G;
XX
DR WPI; 2002-055585/07.
DR P-PSDB; AAU10561.
XX
PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage -
XX
PS Disclosure; Fig 7; 65pp; English.

XX
 CC The invention relates to the use of an insulin-like growth factor I
 CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
 CC of a medicament for treating nerve damage in the peripheral nervous
 CC system, or for treating nerve damage by localising MGF at the site of
 CC damage. The nerve damage may include severing of a nerve. The treatment
 CC may be combined with another treatment (such as a polypeptide growth
 CC factor other than MGF) that prevents or diminishes degeneration of the
 CC target organ (for example, muscle) which the damaged nerve innervates,
 CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
 CC MGF prevents or diminishes degeneration. The method is useful for
 CC treating neurological disorders, preferably motoneuron disorders. These
 CC methods can reduce motoneuron loss by 20% or greater in response to nerve
 CC avulsion. This sequence represents cDNA encoding the rabbit MGF.
 XX
 SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 100.0%; Score 523; DB 24; Length 523;
 Best Local Similarity 100.0%; Pred. No. 5.1e-144;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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 Db 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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 Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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 Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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 Db 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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 Db 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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 Db 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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 Db 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523

RESULT 3

AAT84893

ID AAT84893 standard; cDNA; 553 BP.

XX

AC AAT84893;

XX

DT 14-APR-1998 (first entry)

XX

DE Rabbit insulin like growth factor 1 encoding cDNA.

XX

KW Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;

KW heart; neuromuscular disease; primer; ss.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..366

FT /*tag= a

FT /product= "IGF-1"

XX

PN WO9733997-A1.

XX

PD 18-SEP-1997.

XX

PF 11-MAR-1997; 97WO-GB00658.

XX

PR 11-MAR-1996; 96GB-0005124.

XX

PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.

XX

PI Goldspink G;

XX

DR WPI; 1997-470877/43.

DR P-PSDB; AAW23301.

XX

PT Use of insulin like growth factor I characterised by presence of Ec
PT peptide - to treat humans or animals, particularly muscle disorders,
PT heart conditions or neuromuscular diseases

XX

PS Disclosure; Fig 3; 33pp; English.

XX

CC A use of insulin like growth factor I (IGF-1) has been developed, and
CC is characterised by the presence of the Ec peptide, or a functional
CC equivalent, in the treatment or therapy of a human or animal. The IGF-1
CC polypeptide can be used to treat muscular disorders, e.g. Duchenne or
CC Becker muscular dystrophy, autosomal dystrophies and related progressive
CC skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
CC spinal cord injury induced muscle atrophy and neuromuscular diseases,
CC and cardiac disorders, e.g. diseases where promotion of cardiac muscle
CC protein synthesis is a beneficial treatment, cardiomyopathies and acute
CC heart failure or insult, specifically myocarditis or myocardial
CC infarction. It can also be used to promote bone fracture healing and
CC maintenance of bone in old age. The present sequence encodes rabbit
CC IGF-1 used in the present specification.

XX

SQ Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;

Query Match 100.0%; Score 523; DB 18; Length 553;
 Best Local Similarity 100.0%; Pred. No. 5.3e-144;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db    211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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Db    451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

Qy    481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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```

RESULT 4

AAD06398

ID AAD06398 standard; cDNA; 517 BP.

XX

AC AAD06398;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;

KW sex-linked muscular dystrophy; peripheral neuropathy;
 KW Alzheimer's disease; Parkinson's disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..333
 FT /*tag= a
 FT /product= "Mechano-growth factor (MGF)"
 FT /note= "This region comprises exons 3-6. The CDS does
 FT not include start codon"
 FT /partial
 XX
 PN WO200136483-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-GB04354.
 XX
 PR 15-NOV-1999; 99GB-0026968.
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 PA (UNLO) UNIV COLLEGE LONDON.
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 PI Goldspink G, Johnson I;
 XX
 DR WPI; 2001-355620/37.
 DR P-PSDB; AAE02447.
 XX
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder -
 XX
 PS Claim 4; Page 49-50; 66pp; English.
 XX
 CC The present invention relates to use of mechano-growth factor (MGF),
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneurone loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (Ec) domain, hence also referred as
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.
 XX
 SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 89.4%; Score 467.4; DB 22; Length 517;
 Best Local Similarity 96.2%; Pred. No. 1.3e-127;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
  
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RESULT 5

AAS16877

ID AAS16877 standard; cDNA; 517 BP.

XX

AC AAS16877;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human mechano-growth factor (MGF) cDNA.

XX

KW Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
 KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
 KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
 KW nerve avulsion.

XX

OS Homo sapiens.

```

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FT               /product= "Human MGF"
FT               /partial
FT               /note= "No start codon"
FT   exon          1..76
FT               /*tag= b
FT               /number= 3
FT   exon          77..259
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FT               /number= 5
FT   exon          308..330
FT               /*tag= e
FT               /number= 6
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PN   WO200185781-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-GB02054.
XX
PR   10-MAY-2000; 2000GB-0011278.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
PA   (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI   Goldspink G, Terenghi G;
XX
DR   WPI; 2002-055585/07.
DR   P-PSDB; AAU10559.
XX
PT   Use of insulin-like growth factor I (IGF-I) isoform known as
PT   mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT   ability to reduce motoneuron loss in response to nerve avulsion, to
PT   treat nerve damage -
XX
PS   Claim 11; Fig 5; 65pp; English.
XX
CC   The invention relates to the use of an insulin-like growth factor I
CC   (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC   of a medicament for treating nerve damage in the peripheral nervous
CC   system, or for treating nerve damage by localising MGF at the site of
CC   damage. The nerve damage may include severing of a nerve. The treatment
CC   may be combined with another treatment (such as a polypeptide growth
CC   factor other than MGF) that prevents or diminishes degeneration of the
CC   target organ (for example, muscle) which the damaged nerve innervates,
CC   whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC   MGF prevents or diminishes degeneration. The method is useful for
CC   treating neurological disorders, preferably motorneuron disorders. These
CC   methods can reduce motoneuron loss by 20% or greater in response to nerve
CC   avulsion. This sequence represents cDNA encoding the human MGF.
XX

```

SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 89.4%; Score 467.4; DB 24; Length 517;

Best Local Similarity 96.2%; Pred. No. 1.3e-127;

Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
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Db    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

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Db    358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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Db    417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521
        |||
Db    477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
```

RESULT 6

AAD06405

ID AAD06405 standard; cDNA; 471 BP.

XX

AC AAD06405;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.

XX

KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
 KW sex-linked muscular dystrophy; peripheral neuropathy;
 KW Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.
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 OS *Oryctolagus cuniculus*.
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 FH Key Location/Qualifiers
 FT CDS 1..318
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 FT /transl_except= (pos:7..9, aa:Gln)
 FT /transl_except= (pos:25..27, aa:Gln)
 FT /note= "These translation exceptions occur while decoding
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 FT does not include start codon"
 FT /partial
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 PN WO200136483-A1.
 XX
 PD 25-MAY-2001.
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 PF 15-NOV-2000; 2000WO-GB04354.
 XX
 PR 15-NOV-1999; 99GB-0026968.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 XX
 PI Goldspink G, Johnson I;
 XX
 DR WPI; 2001-355620/37.
 DR P-PSDB; AAE02452, AAE02456.
 XX
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder -
 XX
 PS Disclosure; Page 59-60; 66pp; English.
 XX
 CC The present invention relates to use of mechano-growth factor (MGF),
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneurone loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
 CC The L.IGF-I protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4 and 6.

XX

SQ Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

Query Match 78.2%; Score 409; DB 22; Length 471;

Best Local Similarity 90.1%; Pred. No. 2e-110;

Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

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Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241 ATGCCCAAGACTCAG----- 255

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        |||
Db    256 -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
        |||
Db    309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
        |||
Db    369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
        |||
Db    429 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 471
```

RESULT 7

AAS16884

ID AAS16884 standard; cDNA; 471 BP.

XX

AC AAS16884;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rabbit insulin-like growth factor I liver-type isoform (L.IGF-I) cDNA.

XX

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;

KW nerve avulsion; insulin-like growth factor I liver-type isoform; L.IGF-I;
 XX
 OS Oryctolagus cuniculus.
 XX

FH	Key	Location/Qualifiers
FT	CDS	1..318
FT		/*tag= a
FT		/product= "Rabbit L.IGF-I"
FT		/partial
FT		/note= "No start codon"
FT	exon	1..75
FT		/*tag= b
FT		/number= exon 3
FT	exon	76..258
FT		/*tag= c
FT		/number= exon 4
FT	exon	259..315
FT		/*tag= d
FT		/number= exon 6

XX
 PN WO200185781-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-GB02054.
 XX
 PR 10-MAY-2000; 2000GB-0011278.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
 XX
 PI Goldspink G, Terenghi G;
 XX
 DR WPI; 2002-055585/07.
 DR P-PSDB; AAU10564.
 XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as
 PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
 PT ability to reduce motoneuron loss in response to nerve avulsion, to
 PT treat nerve damage -
 XX

PS Disclosure; Fig 10; 65pp; English.
 XX

CC The invention relates to the use of an insulin-like growth factor I
 CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
 CC of a medicament for treating nerve damage in the peripheral nervous
 CC system, or for treating nerve damage by localising MGF at the site of
 CC damage. The nerve damage may include severing of a nerve. The treatment
 CC may be combined with another treatment (such as a polypeptide growth
 CC factor other than MGF) that prevents or diminishes degeneration of the
 CC target organ (for example, muscle) which the damaged nerve innervates,
 CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
 CC MGF prevents or diminishes degeneration. The method is useful for
 CC treating neurological disorders, preferably motorneuron disorders. These
 CC methods can reduce motoneuron loss by 20% or greater in response to nerve
 CC avulsion. This sequence represents cDNA encoding the rabbit insulin-like
 CC growth factor I liver-type isoform (L.IGF-I) used in experiments on

CC motoneuron loss.

XX

SQ Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

Query Match 78.2%; Score 409; DB 24; Length 471;

Best Local Similarity 90.1%; Pred. No. 2e-110;

Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      |||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db    241 ATGCCCAAGACTCAG----- 255

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db    256 -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db    309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
      |||
Db    429 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 471
```

RESULT 8

AAD06399

ID AAD06399 standard; cDNA; 539 BP.

XX

AC AAD06399;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rat IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Rat; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
 KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
 KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
 KW sex-linked muscular dystrophy; peripheral neuropathy;
 KW Alzheimer's disease; Parkinson's disease; ss.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..336
 FT /*tag= a
 FT /product= "Mechano-growth factor (MGF)"
 FT /note= "This region comprises exons 3-6. The CDS does
 FT not include start codon"
 FT /partial
 XX
 PN WO200136483-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-GB04354.
 XX
 PR 15-NOV-1999; 99GB-0026968.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 XX
 PI Goldspink G, Johnson I;
 XX
 DR WPI; 2001-355620/37.
 DR P-PSDB; AAE02448.
 XX
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder -
 XX
 PS Claim 4; Page 51-52; 66pp; English.
 XX
 CC The present invention relates to use of mechano-growth factor (MGF),
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneurone loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rat IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (Ec) domain, hence also referred as
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.

XX

SQ Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

Query Match 68.2%; Score 356.8; DB 22; Length 539;

Best Local Similarity 82.3%; Pred. No. 5.1e-95;

Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGGCACACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCATCCGGGCCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      ||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGTATC 474
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    421 CTGCTTGAGCAACCTGCAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy    475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
```

RESULT 9

AAS16878

ID AAS16878 standard; cDNA; 539 BP.

XX

AC AAS16878;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rat mechano-growth factor (MGF) cDNA.

XX

KW Rat; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;

KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;

KW muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;

KW nerve avulsion.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /*tag= a

FT /product= "Rat MGF"

FT /partial

FT /note= "No start codon"

FT exon 1..75

FT /*tag= b

FT /number= exon 3

FT exon 76..258

FT /*tag= c

FT /number= exon 4

FT exon 259..309

FT /*tag= d

FT /number= exon 5

FT exon 310..333

FT /*tag= e

FT /number= exon 6

XX

PN WO200185781-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-GB02054.

XX

PR 10-MAY-2000; 2000GB-0011278.

XX

PA (UNLO) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX

PI Goldspink G, Terenghi G;

XX

DR WPI; 2002-055585/07.

DR P-PSDB; AAU10560.

XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage -

XX

PS Disclosure; Fig 6; 65pp; English.

XX

CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motorneuron disorders. These

CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rat MGF.
XX
SQ Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

Query Match 68.2%; Score 356.8; DB 24; Length 539;
Best Local Similarity 82.3%; Pred. No. 5.1e-95;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTTCGGAGGGGCACCACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      |||| | | ||||| |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGGCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      ||||| ||||| ||||| |||| | |||| | |||| | |||| | |||| | ||||
Db    241 ATGCCCAAGACTCAGAAGTCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      ||| ||||| || |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
      || | | ||||| |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy    475 ACATTTCAAAGAT-GGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
      ||||| |||| | ||||| |||| | |||| | |||| | |||| | |||| | ||||
Db    481 TCATTTTCAGAGATGGGCATTTCCTCAATGAAATACACAAGTAAACATTTC 530
```

RESULT 10

ABV76185

ID ABV76185 standard; cDNA; 651 BP.

XX

AC ABV76185;

XX

DT 07-MAR-2003 (first entry)

XX

DE Mouse insulin-like growth factor IB cDNA.

XX

KW Insulin-like growth factor IB; IGF-IB; mouse; mRNA; assay;

KW nucleic acid detection; gene; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 73..474
 FT /*tag= a
 FT /product= "IGF-IB"
 XX
 PN WO200297390-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 31-MAY-2002; 2002WO-SE01056.
 XX
 PR 01-JUN-2001; 2001SE-0001934.
 XX
 PA (BIOV-) BIOVITRUM AB.
 XX
 PI Parrow V, Rosengren L;
 XX
 DR WPI; 2003-129529/12.
 XX
 PT Quantitating a target nucleic acid in a sample comprises immobilizing,
 PT on a solid support, a sample comprising a target nucleic acid, and
 PT detecting and quantitating signals generated from the antisense and
 PT sense probes -
 XX
 PS Example 1; Page 16-17; 18pp; English.
 XX
 CC The present sequence is that of cDNA encoding murine insulin-like
 CC growth factor 1B (IGF-IB). The cDNA was used in an example of the
 CC method of the invention to generate probes for determination of
 CC IGF-IB RNA. The method comprises a quantitative hybridisation
 CC assay for analysis of mRNA in a target nucleic acid (TNA) sample.
 CC It involves: (i) immobilising the TNA sample on a solid support;
 CC (ii) contacting a labelled antisense probe to a first portion of the
 CC TNA, and a labelled sense probe to a second portion of the TNA;
 CC (iii) detecting and quantitating the signals generated from the
 CC hybridised probes; and (iv) determining the value represented by
 CC the antisense probe signal minus the sense probe signal, the value
 CC being proportional to the amount of mRNA in the TNA sample. In an
 CC example of the method, a cDNA clone containing 60 nucleotides from
 CC exon 2 and 179 nucleotides from exon 3 of the mouse IGF-IB gene was
 CC cloned into pGEN-4Z vector. Linearisation of the plasmid with
 CC EcoRI allowed transcription of a 250-nucleotide antisense probe
 CC using T7 polymerase. Linearisation with HindIII allowed
 CC transcription of a sense probe of similar length using SP6
 CC polymerase (see ABV76186). The probes were purified and used to
 CC determine IGF-I RNA in mouse hepatocytes and also in rat hepatocytes.
 XX
 SQ Sequence 651 BP; 193 A; 185 C; 149 G; 124 T; 0 other;

 Query Match 66.8%; Score 349.4; DB 25; Length 651;
 Best Local Similarity 82.8%; Pred. No. 8.3e-93;
 Matches 425; Conservative 0; Mismatches 81; Indels 7; Gaps 2;

XX
 PR 20-NOV-1986; 86US-0929671.
 PR 07-JAN-1986; 86US-0816662.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Krivi GG, Rotwein PS;
 XX
 DR WPI; 1987-200203/29.
 XX
 PT New pre-pro-insulin-like growth factor-1 protein - obtd. by
 PT recombinant DNA procedures for use as growth promoters for
 PT enhancing lactation, for stimulating cell proliferation etc.
 XX
 PS Example; Fig 5; 59pp; English.
 XX
 CC A 42 base oligonucleotide corresponding to the DNA sequence encoding
 CC amino acids 10 to 23 of mature human IGF-I was synthesized (AAN70437).
 CC The radiolabeled 42 mer was then employed to screen for IGF-I
 CC containing DNA sequences in a human liver cDNA library. Insulin-
 CC like growth factors-1A and -1B cDNAs were isolated from a human cDNA
 CC library by using lambdagt 11 (AAN70435, AAN70436). The human IGF-1
 CC genomic gene was isolated and mapped. It encodes at least two
 CC preproinsulin-like growth factor-1 proteins. An essentially pure
 CC preproinsulin-like growth factor-1 protein comprising the sequence
 CC of amino acids shown in Figure six is claimed (AAP70277).
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;

Query Match 63.9%; Score 334.4; DB 8; Length 818;
 Best Local Similarity 84.6%; Pred. No. 2.4e-88;
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 203 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 262
 Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
 |||||||||||||||||||||||||||||||||||||||| || |||||||||||||||||||| |||||
 Db 263 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 322
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
 Db 323 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 382
 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
 || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||
 Db 383 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 442
 Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 |||||||||| |||
 Db 443 ATGCCCAAGACCCAG----- 457
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
 Db 458 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 510

CC The methods are also useful as a screening tool for agents that modulate
 CC the onset or progression of breast cancer. The breast cancer genes may be
 CC used as diagnostic markers for the prediction or identification of the
 CC malignant state of breast tissue, for confirming the type and progression
 CC of cancer, and for drug screening and assays. The present sequence is a
 CC coding sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub.published_pct_sequences.
 XX
 SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
 Best Local Similarity 84.6%; Pred. No. 5.7e-88;
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
          |||
Db      371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||
Db      431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
          |||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||
Db      551 ATGCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          |||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
          |||
Db      619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
          |||
Db      679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACAT 738

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
          |||
Db      739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784

```

RESULT 13
 ABK84583
 ID ABK84583 standard; cDNA; 7260 BP.
 XX

AC ABK84583;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #1154.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
PR 03-OCT-2000; 2000US-237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID No 1154; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)

CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
 Best Local Similarity 84.6%; Pred. No. 5.7e-88;
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60
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Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db     566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db     619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
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Db     679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACAT 738

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523

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Db || ||||| ||| ||||||||||||||||||||||||||||
739 TTAAAGATGGGCGTTTCCCCAATGAAATACACAAGTAAACATTC 784

RESULT 14

ABN97244

ID ABN97244 standard; DNA; 7260 BP.

XX

AC ABN97244;

XX

DT 13-AUG-2002 (first entry)

XX

DE Gene #3742 used to diagnose liver cancer.

XX

KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;

KW metastatic liver tumour; cytostatic; expression profile; disease state;

KW disease progression; drug toxicity; drug efficacy; drug metabolism.

XX

OS Homo sapiens.

XX

PN WO200229103-A2.

XX

PD 11-APR-2002.

XX

PF 02-OCT-2001; 2001WO-US30589.

XX

PR 02-OCT-2000; 2000US-237054P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX

DR WPI; 2002-426119/45.

XX

PT Diagnosing and detecting the progression of liver cancer,

PT hepatocellular carcinoma or metastatic liver tumor in a patient,

PT involves detecting the level of expression of two or more genes in a

PT liver tissue sample -

XX

PS Claim 1; SEQ ID NO 3742; 298pp; English.

XX

CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
Best Local Similarity 84.6%; Pred. No. 5.7e-88;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db    311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Qy     361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db    619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db    679 CTCTGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
      ||
Db    739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
```

RESULT 15

ABK64812

ID ABK64812 standard; DNA; 7260 BP.

XX

AC ABK64812;

XX

DT 18-JUN-2002 (first entry)

XX

DE Human benign prostatic hyperplasia gene #707.

XX

KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200212440-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 07-AUG-2001; 2001WO-US24708.
 XX
 PR 07-AUG-2000; 2000US-223323P.
 PR 05-JUN-2001; 2001US-0873319.
 XX
 PA (GENE-) GENE LOGIC INC.
 PA (NISB) JAPAN TOBACCO INC.
 XX
 PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
 XX
 DR WPI; 2002-257476/30.
 XX
 PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
 PT detecting expression levels of one or more genes in prostate cells from
 PT patient that are differentially regulated compared to normal prostate
 PT cells -
 XX
 PS Disclosure; Page 391-393; 444pp; English.
 XX
 CC The invention relates to a method of diagnosing (I) the onset or
 CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
 CC or identifying an agent that modulates the onset or progression of BPH.
 CC The method is based on changes in gene expression in BPH tissue isolated
 CC from patients exhibiting different clinical states of prostate
 CC hyperplasia as compared to normal prostate tissue. (I) comprises
 CC detecting the expression levels of one or more genes in prostate cells
 CC from the subject that are differentially regulated compared to normal
 CC prostate cells. (II) comprises preparing a first gene expression profile
 CC of BPH cells or BPH-like cell population, exposing the cells to the
 CC agent, preparing a second gene expression profile of the agent exposed
 CC cells, and comparing the first and second gene expression profiles.
 CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
 CC useful for identifying an agent that modulates the onset or progression
 CC of BPH. The methods are useful to present information identifying
 CC the expression level in a tissue or cells, by comparing the expression
 CC level of genes given in the specification in the tissue or cells to the
 CC level of expression of gene in the database, and displaying the
 CC expression levels of at least one gene in the tissue or cell sample
 CC compared to the expression level in BPH. Agents using (II) are useful for
 CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
 CC benign prostatic hyperplasia gene sequences of the invention.
 XX
 SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

 Query Match 63.9%; Score 334.4; DB 24; Length 7260;
 Best Local Similarity 84.6%; Pred. No. 5.7e-88;
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

 Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 ||||||||||||||||||| |||||||||||||||||||
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 Qy 61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120

```

Db      371  AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430
Qy      121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Db      431  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
Qy      181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
Db      491  TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550
Qy      241  ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Db      551  ATGCCCCAAGACCCAG----- 565
Qy      301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Db      566  -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618
Qy      361  CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
Db      619  CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678
Qy      421  CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
Db      679  CTCTGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738
Qy      479  TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
Db      739  TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784

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Job time : 211.995 secs

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 06:03:55 ; Search time 48.3585 Seconds
(without alignments)
4773.589 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	523	100.0	553	3	US-09-142-583A-3	Sequence 3, Appli
2	523	100.0	553	3	US-09-142-583A-5	Sequence 5, Appli
3	332.8	63.6	777	3	US-09-142-583A-10	Sequence 10, Appl
4	331.2	63.3	622	6	5405942-2	Patent No. 5405942
5	274.6	52.5	5707	2	US-08-472-809B-8	Sequence 8, Appli
6	274.6	52.5	6345	2	US-08-472-809B-7	Sequence 7, Appli
7	234.4	44.8	357	6	5405942-13	Patent No. 5405942
8	232.8	44.5	357	6	5405942-9	Patent No. 5405942
9	191.4	36.6	210	6	5405942-7	Patent No. 5405942
10	191.4	36.6	210	6	5405942-11	Patent No. 5405942
11	191.4	36.6	2862	4	US-09-255-829-13	Sequence 13, Appl

12	189.8	36.3	210	6	5405942-15	Patent No. 5405942
13	185.2	35.4	240	1	US-08-308-196A-1	Sequence 1, Appli
14	185.2	35.4	240	5	PCT-US91-06452-1	Sequence 1, Appli
15	185.2	35.4	390	3	US-09-029-267-13	Sequence 13, Appl
16	158.8	30.4	798	1	US-07-953-230A-6	Sequence 6, Appli
17	154.8	29.6	770	1	US-07-953-230A-1	Sequence 1, Appli
18	154.8	29.6	846	1	US-07-953-230A-5	Sequence 5, Appli
19	127	24.3	621	3	US-08-989-251-40	Sequence 40, Appl
20	127	24.3	621	3	US-09-340-250-40	Sequence 40, Appl
21	127	24.3	621	4	US-09-528-108-40	Sequence 40, Appl
22	125.8	24.1	233	1	US-08-444-142-3	Sequence 3, Appli
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24	125.8	24.1	485	1	US-07-989-845-29	Sequence 29, Appl
25	125.8	24.1	485	1	US-07-989-844-13	Sequence 13, Appl
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32	125.8	24.1	485	1	US-08-385-187A-1	Sequence 1, Appli
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34	125.8	24.1	485	5	PCT-US93-11297-13	Sequence 13, Appl
35	125.8	24.1	485	5	PCT-US93-11298-29	Sequence 29, Appl
36	125.6	24.0	243	2	US-08-482-182-75	Sequence 75, Appl
37	124.2	23.7	717	1	US-08-284-784-40	Sequence 40, Appl
38	124.2	23.7	717	2	US-08-854-811-40	Sequence 40, Appl
39	124.2	23.7	783	1	US-08-284-784-43	Sequence 43, Appl
40	124.2	23.7	783	2	US-08-854-811-43	Sequence 43, Appl
41	124.2	23.7	891	1	US-08-284-784-33	Sequence 33, Appl
42	124.2	23.7	891	1	US-08-284-784-34	Sequence 34, Appl
43	124.2	23.7	891	2	US-08-854-811-33	Sequence 33, Appl
44	124.2	23.7	891	2	US-08-854-811-34	Sequence 34, Appl
45	124.2	23.7	900	1	US-08-284-784-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-142-583A-3

; Sequence 3, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/142,583A
;      FILING DATE: 29-Oct-1998
;      CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: WO PCT/GB97/00658
;      FILING DATE: 11-MAR-1997
;      APPLICATION NUMBER: GB 9605124.8
;      FILING DATE: 11-MAR-1996
;
; ATTORNEY/AGENT INFORMATION:
;      NAME: SADOFF, B. J.
;      REGISTRATION NUMBER: 36663
;      REFERENCE/DOCKET NUMBER: 117-263
;
; TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 7038164000
;      TELEFAX: 7038164100
;
; INFORMATION FOR SEQ ID NO: 3:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 553 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: both
;          TOPOLOGY: linear
;      MOLECULE TYPE: cDNA
;      FEATURE:
;          NAME/KEY: CDS
;          LOCATION: 1..363
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;      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-142-583A-3

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Query Match          100.0%;  Score 523;  DB 3;  Length 553;
Best Local Similarity 100.0%;  Pred. No. 1.6e-154;
Matches 523;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      31  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy      61  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      91  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

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Qy 481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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Db 511 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553

RESULT 2

US-09-142-583A-5

; Sequence 5, Application US/09142583A
 ; Patent No. 6221842
 ; GENERAL INFORMATION:
 ; APPLICANT: GOLDSPIK, GEOFFREY
 ; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/142,583A
 ; FILING DATE: 29-Oct-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/GB97/00658
 ; FILING DATE: 11-MAR-1997
 ; APPLICATION NUMBER: GB 9605124.8
 ; FILING DATE: 11-MAR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SADOFF, B. J.
 ; REGISTRATION NUMBER: 36663
 ; REFERENCE/DOCKET NUMBER: 117-263
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 7038164000
 ; TELEFAX: 7038164100
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 553 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear

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;      MOLECULE TYPE: cDNA
;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: 341..397
;      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-142-583A-5

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Query Match          100.0%; Score 523; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-154;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      91 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 270

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy     361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy     421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

Qy     481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553

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RESULT 3

US-09-142-583A-10

; Sequence 10, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:


```

;      ADDRESSEE: NIXON & VANDERHYE P.C.
;      STREET: 1100 NORTH GLEBE ROAD
;      CITY: ARLINGTON
;      STATE: VA
;      COUNTRY: USA
;      ZIP: 22201
;
;  COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;
;  CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/142,583A
;      FILING DATE: 29-Oct-1998
;      CLASSIFICATION: <Unknown>
;
;  PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: WO PCT/GB97/00658
;      FILING DATE: 11-MAR-1997
;      APPLICATION NUMBER: GB 9605124.8
;      FILING DATE: 11-MAR-1996
;
;  ATTORNEY/AGENT INFORMATION:
;      NAME: SADOFF, B. J.
;      REGISTRATION NUMBER: 36663
;      REFERENCE/DOCKET NUMBER: 117-263
;
;  TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 7038164000
;      TELEFAX: 7038164100
;
;  INFORMATION FOR SEQ ID NO: 10:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 777 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: both
;          TOPOLOGY: linear
;
;      MOLECULE TYPE: cDNA
;      FEATURE:
;          NAME/KEY: CDS
;          LOCATION: 26..493
;
;      SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-142-583A-10

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Query Match          63.6%;  Score 332.8;  DB 3;  Length 777;
Best Local Similarity 84.4%;  Pred. No. 9.8e-95;
Matches 444;  Conservative 0;  Mismatches 27;  Indels 55;  Gaps 4;

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Qy      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||||||||||||||| ||||||||||||||||||||||||||||||||
Db      179 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 238

Qy      61  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
          |||||||||||||||| || |||||||||||||||| |||||
Db      239 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 298

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          ||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db      299 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 358

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

```


Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
 :| |||||:||||| || ||| |||| |||:| |:|:|:||||| |||||
 Db 225 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGCUCUGUCCGUGCCCAGCGCCACACCGAC 284
 Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 |:||||| |||
 Db 285 AUGCCCAAGACCCAG----- 299
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||||:|:|:|:| ||||:|||||:||||| |||||:|
 Db 300 -----AAGGAAGUACAUUUGAAGAACGCAAGUAGAGGGAGUGCAGGAAACAAGAACUA 352
 Qy 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
 ||||:|:|||||: |:||||:|||| ||| ||||| |||:|
 Db 353 CAGGAUGUAGGAAGACCCUCCUGAGGAGUGAAGAGUGACAUGCCACCGCAGGAUCCUUUG 412
 Qy 421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
 |:|:|||| |:|:|:| :||| ::||| ||| |||||:|:|:|:|:|:|
 Db 413 CUCUGCACGAGUUACCUGUUAACUUUGGAACACCUACCAAAAAUAAGUUUGAUAAACAU 472
 Qy 479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
 :: ||||: ||| ::|:|||||:||||:|||||:||||:|
 Db 473 UUAAGAUGGGCGUUUCCCCCAUGAAAUACACAAGUAAACAUUC 518

RESULT 5

US-08-472-809B-8

; Sequence 8, Application US/08472809B
 ; Patent No. 5925564
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwartz, Robert J.
 ; APPLICANT: DeMayo, Franco J.
 ; APPLICANT: O'Malley, Bert W.
 ; TITLE OF INVENTION: Expression Vector Systems and
 ; TITLE OF INVENTION: Method of Use
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/472,809B
 ; FILING DATE: June 7, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/209,846

```

; FILING DATE: March 9, 1994
; APPLICATION NUMBER: 07/789,919
; FILING DATE: No. 5925564ember 6, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 214/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5707 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-472-809B-8

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Query Match          52.5%; Score 274.6; DB 2; Length 5707;
Best Local Similarity 82.2%; Pred. No. 5.3e-76;
Matches 351; Conservative 0; Mismatches 24; Indels 52; Gaps 1;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      793 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 852

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
          |||
Db      853 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 912

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||
Db      913 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 972

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
          || |||
Db      973 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 1032

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||
Db      1033 ATGCCCAAGACCCAG----- 1047

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          |||
Db      1048 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 1100

Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
          |||
Db      1101 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCG 1160

Qy      421 CTCTGCA 427
          |||
Db      1161 GGCTGCA 1167

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RESULT 6
 US-08-472-809B-7
 ; Sequence 7, Application US/08472809B
 ; Patent No. 5925564
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwartz, Robert J.
 ; APPLICANT: DeMayo, Franco J.
 ; APPLICANT: O'Malley, Bert W.
 ; TITLE OF INVENTION: Expression Vector Systems and
 ; TITLE OF INVENTION: Method of Use
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/472,809B
 ; FILING DATE: June 7, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/209,846
 ; FILING DATE: March 9, 1994
 ; APPLICATION NUMBER: 07/789,919
 ; FILING DATE: No. 5925564ember 6, 1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 214/212
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6345 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-08-472-809B-7

Query Match 52.5%; Score 274.6; DB 2; Length 6345;
 Best Local Similarity 82.2%; Pred. No. 5.6e-76;
 Matches 351; Conservative 0; Mismatches 24; Indels 52; Gaps 1;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      3702 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 3761
Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
        ||||||||||||||||||||||||||||| || ||||||||||||||||||| |||||
Db      3762 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 3821
Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        ||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||
Db      3822 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 3881
Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
        || ||||||||||||||| || ||| |||| ||||| |||||||||||||||||||
Db      3882 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 3941
Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        ||||||||||| |||
Db      3942 ATGCCCAAGACCCAG----- 3956
Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        ||||||||||||||||||| ||||||||||||||||||| |||||||||||
Db      3957 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 4009
Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420
        ||||||||||||||||||| ||||||||||||||| |||| ||||||||||| || |
Db      4010 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCG 4069
Qy      421 CTCTGCA 427
        |||||
Db      4070 GGCTGCA 4076

```

RESULT 7

5405942-13

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:13:

; LENGTH: 357

5405942-13

Query Match 44.8%; Score 234.4; DB 6; Length 357;

Best Local Similarity 93.8%; Pred. No. 5.1e-64;

Matches 244; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        ||||||||||||||||||| ||||||||||||||||||| |||||||||||
Db      43 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 102

```

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Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
      |||
Db      103 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 162

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      163 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 222

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      ||
Db      223 TGCACACCCCTCAGGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 282

Qy      241 ATGCCCCAAGACTCAGAAGTA 260
      |||
Db      283 ATGCCCCAAGACCCAGAAGGA 302

```

RESULT 8

5405942-9

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

; SEQ ID NO: 9:

; LENGTH: 357

5405942-9

Query Match 44.5%; Score 232.8; DB 6; Length 357;
Best Local Similarity 76.5%; Pred. No. 1.6e-63;
Matches 199; Conservative 44; Mismatches 17; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      43 GGACCGGAGACGCUCUGCGGGGUGAGCUGGUGGACGCUCUUCAGUUCGUGUGGAGAC 102

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
      |||
Db      103 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGGCGCCUCAG 162

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      163 ACAGGUAUCGUGGAUGAGUGCUGUUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 222

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      :|
Db      223 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGCUCUGUCCGUGCCCAGCGCCACACCGAC 282

Qy      241 ATGCCCCAAGACTCAGAAGTA 260
      |:|

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; LENGTH: 210
5405942-11

Query Match 36.6%; Score 191.4; DB 6; Length 210;
Best Local Similarity 94.7%; Pred. No. 1.2e-50;
Matches 198; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
          |||
Db     61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||
Db    121 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
          ||
Db    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGC 209
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RESULT 11

US-09-255-829-13

; Sequence 13, Application US/09255829

; Patent No. 6461617

; GENERAL INFORMATION:

; APPLICANT: Shone, Clifford Charles

; APPLICANT: Quinn, Conrad Padraig

; APPLICANT: Foster, Keith Alan

; TITLE OF INVENTION: Recombinant Toxin Fragments

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/255,829

; FILING DATE: 23-FEB-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB97/02273

; FILING DATE: 22-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/782,893

; FILING DATE: 27-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: ESMOND, ROBERT W.

```

;      REGISTRATION NUMBER: 32,893
;      REFERENCE/DOCKET NUMBER: 1581.0130002
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 202-371-2600
;      TELEFAX: 202-371-2540
;      INFORMATION FOR SEQ ID NO: 13:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 2862 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;      MOLECULE TYPE: DNA (genomic)
;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: 1..2862
US-09-255-829-13

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Query Match          36.6%; Score 191.4; DB 4; Length 2862;
Best Local Similarity 94.7%; Pred. No. 4.8e-50;
Matches 198; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      2644 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 2703

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
      |||
Db      2704 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 2763

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      2764 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 2823

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
      ||
Db      2824 TGCGCACCCCTCAAGCCTGCCAAGTCAGC 2852

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RESULT 12
5405942-15
;Patent No. 5405942
;  APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;  TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;  NUMBER OF SEQUENCES: 16
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/07/65,673
;    FILING DATE: 16-JUN-1987
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 630,557
;    FILING DATE: 19-JUL-1984
;SEQ ID NO:15:
;  LENGTH: 210
5405942-15

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Query Match          36.3%; Score 189.8; DB 6; Length 210;

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Best Local Similarity 74.6%; Pred. No. 3.8e-50;
Matches 156; Conservative 41; Mismatches 12; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||:|||||:|:|||| ||:||||:|:||||:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 GGACCGGAGACGCUCUGCGGGGCGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
        |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     61 AGGGGCUUUUAUUUCAACAAGCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        |||| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    121 ACAGGUAUCGUGGAUGAGUGCUGCUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
        :| |||:|:|:|:| || || || || ||
Db    181 UGCGCACCCUCAGGCCUGCCAAGUCAGC 209
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RESULT 13

US-08-308-196A-1

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; Sequence 1, Application US/08308196A
; Patent No. 5612198
; GENERAL INFORMATION:
;   APPLICANT: Brierley, Russell A.
;   APPLICANT: Davis, Geneva R.
;   APPLICANT: Holtz, Gregory C.
;   APPLICANT: Gleeson, Martin A.
;   APPLICANT: Howard, Bradley D.
;   TITLE OF INVENTION: Production of Insulin-Like Growth
;   TITLE OF INVENTION: Factor-1 in Methylophilic Yeast Cells
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Brown, Martin, Haller & McClain
;     STREET: 1660 Union Street
;     CITY: San Diego
;     STATE: California
;     COUNTRY: USA
;     ZIP: 92101-2926
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/308,196A
;     FILING DATE: 09-SEPT-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/983,523
;     FILING DATE: 03-MAR-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/578,728
;     FILING DATE: 04-SEP-1990
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Seidman, Stephanie L.
;     REGISTRATION NUMBER: 33,779
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; REFERENCE/DOCKET NUMBER: 51875
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..232
US-08-308-196A-1

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Best Local Similarity 91.6%; Pred. No. 1.1e-48;
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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; Sequence 1, Application PC/TUS9106452
; GENERAL INFORMATION:
; APPLICANT: Brierley, Russell A.
; APPLICANT: Davis, Geneva R.
; APPLICANT: Holtz, Gregory C.
; APPLICANT: Gleeson, Martin A.
; APPLICANT: Bradley, D. H.
; TITLE OF INVENTION: Production of Insulin-Like Growth
; TITLE OF INVENTION: Factor-1 in Methyloleophilic Yeast Cells
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/06452
; FILING DATE: 19910409
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/578,728
; FILING DATE: 04-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 51874
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..232
PCT-US91-06452-1

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Query Match          35.4%; Score 185.2; DB 5; Length 240;
Best Local Similarity 91.6%; Pred. No. 1.1e-48;
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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RESULT 15

US-09-029-267-13

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; Sequence 13, Application US/09029267
; Patent No. 6107057
; GENERAL INFORMATION:
; APPLICANT: Crawford, Kenneth
; APPLICANT: Zaror, Isabel

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; APPLICANT: Innis, Michael
; TITLE OF INVENTION: Pichia Secretory Leader for Protein
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: United States
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,267
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chung, Ling-Fong
; REGISTRATION NUMBER: 36,482
; REFERENCE/DOCKET NUMBER: 1165.100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2704
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"

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US-09-029-267-13

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Best Local Similarity 91.6%; Pred. No. 1.5e-48;
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Db      280 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 339

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Job time : 49.3585 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:29:55 ; Search time 233.512 Seconds
(without alignments)
7443.919 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	409	78.2	471	9	US-09-852-261-13	Sequence 13, Appl
4	356.8	68.2	539	9	US-09-852-261-3	Sequence 3, Appli
5	349.4	66.8	651	15	US-10-161-088-1	Sequence 1, Appli
6	334.4	63.9	7260	10	US-09-919-497-24	Sequence 24, Appl
7	334.4	63.9	7260	10	US-09-880-107-3739	Sequence 3739, Ap
8	334.4	63.9	7260	13	US-09-873-319-707	Sequence 707, App
9	334.4	63.9	7260	13	US-09-960-706-1066	Sequence 1066, Ap
10	334.4	63.9	7260	15	US-10-136-639-4	Sequence 4, Appli
11	332.8	63.6	725	15	US-10-207-655-54	Sequence 54, Appl
12	273.6	52.3	612	13	US-10-251-661-7	Sequence 7, Appli
13	262	50.1	487	9	US-09-852-261-11	Sequence 11, Appl
14	237.6	45.4	318	9	US-09-852-261-9	Sequence 9, Appli
15	228	43.6	462	15	US-10-238-114-1	Sequence 1, Appli
16	209	40.0	286	15	US-10-161-088-3	Sequence 3, Appli
17	193	36.9	210	13	US-09-807-742-18	Sequence 18, Appl
18	191.4	36.6	2862	13	US-10-241-596-13	Sequence 13, Appl
19	187	35.8	4532	10	US-09-930-377B-1	Sequence 1, Appli
20	186.6	35.7	210	10	US-09-930-377B-2	Sequence 2, Appli
21	185.2	35.4	390	15	US-10-179-046-13	Sequence 13, Appl
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24	141.6	27.1	213	15	US-10-076-816-9	Sequence 9, Appli
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28	113.4	21.7	480	9	US-09-921-398-38	Sequence 38, Appl
29	113.4	21.7	480	15	US-10-280-826-38	Sequence 38, Appl
30	101.8	19.5	210	13	US-09-807-742-19	Sequence 19, Appl
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c 32	75.4	14.4	447	9	US-09-922-217-917	Sequence 917, App
c 33	75.4	14.4	447	10	US-09-833-263-917	Sequence 917, App
c 34	75.4	14.4	447	14	US-10-025-380-917	Sequence 917, App
c 35	75.2	14.4	437	15	US-10-066-543-663	Sequence 663, App
c 36	75.2	14.4	493	15	US-10-066-543-997	Sequence 997, App
c 37	75.2	14.4	518	15	US-10-066-543-1040	Sequence 1040, Ap
c 38	75.2	14.4	536	15	US-10-066-543-428	Sequence 428, App
39	75.2	14.4	543	15	US-10-136-841-1	Sequence 1, Appli
c 40	75.2	14.4	549	15	US-10-066-543-478	Sequence 478, App
c 41	75.2	14.4	574	9	US-09-922-217-918	Sequence 918, App
c 42	75.2	14.4	574	10	US-09-833-263-918	Sequence 918, App
c 43	75.2	14.4	574	14	US-10-025-380-918	Sequence 918, App
c 44	75.2	14.4	577	15	US-10-066-543-1137	Sequence 1137, Ap
c 45	75.2	14.4	579	15	US-10-066-543-1094	Sequence 1094, Ap

ALIGNMENTS

RESULT 1

US-09-852-261-5

; Sequence 5, Application US/09852261

; Patent No. US20020083477A1

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

```
; APPLICANT:  TERENGHI, GIORGIO
; TITLE OF INVENTION:  REPAIR OF NERVE DAMAGE
; FILE REFERENCE:  117-351
; CURRENT APPLICATION NUMBER:  US/09/852,261
; CURRENT FILING DATE:  2001-05-10
; PRIOR APPLICATION NUMBER:  GB 0011278.9
; PRIOR FILING DATE:  2000-05-10
; NUMBER OF SEQ ID NOS:  14
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH:  523
;   TYPE:  DNA
;   ORGANISM:  Oryctolagus cuniculus
US-09-852-261-5
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Query Match          100.0%;  Score 523;  DB 9;  Length 523;
Best Local Similarity 100.0%;  Pred. No. 1.9e-161;
Matches 523;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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RESULT 2

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; Sequence 1, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-261-1

Query Match 89.4%; Score 467.4; DB 9; Length 517;
Best Local Similarity 96.2%; Pred. No. 3.8e-143;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
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Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Db	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC	240
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
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Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	480
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RESULT 3

US-09-852-261-13

; Sequence 13, Application US/09852261

; Patent No. US20020083477A1

; GENERAL INFORMATION:

; APPLICANT: GOLDSPINK, GEOFFREY

; APPLICANT: TERENGHI, GIORGIO

; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE

; FILE REFERENCE: 117-351

; CURRENT APPLICATION NUMBER: US/09/852,261

; CURRENT FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: GB 0011278.9

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 471

; TYPE: DNA

; ORGANISM: Oryctolagus cuniculus

US-09-852-261-13

Query Match 78.2%; Score 409; DB 9; Length 471;

Best Local Similarity 90.1%; Pred. No. 6.1e-124;

Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

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Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

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Db 309 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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 Db 369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
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RESULT 4

US-09-852-261-3
 ; Sequence 3, Application US/09852261
 ; Patent No. US20020083477A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GOLDSPIK, GEOFFREY
 ; APPLICANT: TERENCE, GIORGIO
 ; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
 ; FILE REFERENCE: 117-351
 ; CURRENT APPLICATION NUMBER: US/09/852,261
 ; CURRENT FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: GB 0011278.9
 ; PRIOR FILING DATE: 2000-05-10
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 539
 ; TYPE: DNA
 ; ORGANISM: Rattus sp.
 US-09-852-261-3

Query Match 68.2%; Score 356.8; DB 9; Length 539;
 Best Local Similarity 82.3%; Pred. No. 9.9e-107;
 Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 |||
 Db 1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
 |||
 Db 61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTTCGGAGGGCACACAG 120

Qy 121 ACAGGCATCGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 ||
 Db 121 ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
 |||
 Db 181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCATCCGGGCCAGCGCCACACTGAC 240

Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 |||
 Db 241 ATGCCCAAGACTCAGAAGTCCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||
 Db 301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

```

Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      ||| ||||| || ||| | |||| | || | || | ||||| || |||||
Db      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCAACGCAAGATCCTTTG 420

Qy      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
      || | ||||| |||| ||| |||| | || ||| |||| ||
Db      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy      475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      ||||| |||| ||||| ||||| ||||| ||||| ||||| |||||
Db      481 TCATTTCAAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 530

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RESULT 5

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US-10-161-088-1
; Sequence 1, Application US/10161088
; Publication No. US20030077761A1
; GENERAL INFORMATION:
; APPLICANT: Parrow, Vendela
; APPLICANT: Rosengren, Linda
; TITLE OF INVENTION: NEW METHODS
; FILE REFERENCE: 13425-111001
; CURRENT APPLICATION NUMBER: US/10/161,088
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: SE 0101934-8
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(471)
US-10-161-088-1

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Query Match          66.8%; Score 349.4; DB 15; Length 651;
Best Local Similarity 82.8%; Pred. No. 3e-104;
Matches 425; Conservative 0; Mismatches 81; Indels 7; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60
      ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      139 GGACAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGACCG 198

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      199 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTTCGGAGGGGCACCTCAG 258

Qy      121 ACAGGCATCGTGGATGAGTGTCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      259 ACAGGCATTGTGGATGAGTGTCTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      ||||| || || ||||| |||| ||||| ||||| ||||| ||||| |||||
Db      319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCAGCGCCACACTGAC 378

```

Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 |||||
 Db 379 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438

Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||||
 Db 439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498

Qy 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
 ||| ||||| || ||| | ||| | || | || ||||| |||||
 Db 499 CAGAATGTAGGAGGAGCCTCCACGAGCAGAAAATGCCACATCACC GCAGGATCCTTTG 558

Qy 421 CTCTGCACAGTTACCTGTAAACATTTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
 || | ||||| | || ||| ||| || ||||| ||
 Db 559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618

Qy 475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 506
 ||||| ||||| |||||
 Db 619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651

RESULT 6

US-09-919-497-24

; Sequence 24, Application US/09919497
 ; Patent No. US20020106662A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mutter, George L.
 ; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
 ; FILE REFERENCE: B0801/7225
 ; CURRENT APPLICATION NUMBER: US/09/919,497
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: US 60/221,735
 ; PRIOR FILING DATE: 2000-07-31
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 7260
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-919-497-24

Query Match 63.9%; Score 334.4; DB 10; Length 7260;
 Best Local Similarity 84.6%; Pred. No. 9e-99;
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 |||||
 Db 311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy 61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
 |||||
 Db 371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 430

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 |||||
 Db 431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

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Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      || ||||| ||||| || ||| |||| ||||| ||||| ||||| ||||| |||||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      ||||| ||||| |||
Db      551 ATGCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      ||||| ||||| ||||| ||||| ||||| ||| ||||| ||||| ||||| |||||
Db      679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
      || ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784

```

RESULT 7

US-09-880-107-3739

; Sequence 3739, Application US/09880107

; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.

; APPLICANT: Vockley, Joseph G.

; APPLICANT: Scherf, Uwe

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44921-5028-WO

; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/211,379

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/237,054

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 3950

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3739

; LENGTH: 7260

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025

US-09-880-107-3739

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Query Match          63.9%; Score 334.4; DB 10; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```


Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 |||
 Db 311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
 |||
 Db 371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 |||
 Db 431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
 || |||
 Db 491 TGCACACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 |||
 Db 551 ATGCCCAAGACCCAG----- 565

Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTA 360
 |||
 Db 566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGAGGAAACAAGAACTA 618

Qy 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
 |||
 Db 619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy 421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
 |||
 Db 679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy 479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
 || |||
 Db 739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784

RESULT 8

US-09-873-319-707

; Sequence 707, Application US/09873319A

; Publication No. US20030134324A1

; GENERAL INFORMATION:

; APPLICANT: Munger, William E.

; APPLICANT: Kulkarni, Prakash

; APPLICANT: Getzenberg, Robert H.

; APPLICANT: Waga, Iwao

; APPLICANT: Yamamoto, Jun

; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic

; TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles

; FILE REFERENCE: 44921-5029-US

; CURRENT APPLICATION NUMBER: US/09/873,319A

; CURRENT FILING DATE: 2001-06-05

; EARLIER APPLICATION NUMBER: US 60/223,323

; EARLIER FILING DATE: 2000-08-07

; NUMBER OF SEQ ID NOS: 755

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 707

; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 X57025
US-09-873-319-707

Query Match 63.9%; Score 334.4; DB 13; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
          |||
Db      371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
          ||
Db     491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||
Db     551 ATGCCCAAGACCCAG----- 565

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          |||
Db     566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
          |||
Db     619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
          |||
Db     679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
          ||
Db     739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
```

RESULT 9

US-09-960-706-1066

; Sequence 1066, Application US/09960706

; Publication No. US20030134280A1

; GENERAL INFORMATION:

; APPLICANT: Munger, William E.

; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia Using

; TITLE OF INVENTION: Gene Expression Profiles

```
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1066
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X57025
US-09-960-706-1066
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Query Match          63.9%; Score 334.4; DB 13; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;
```

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
          |||
Db      371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 430

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||
Db      431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
          || |||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||
Db      551 ATGCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          |||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
          |||
Db      619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
          |||
Db      679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
          ||
Db      739 TTTAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
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RESULT 10
 US-10-136-639-4
 ; Sequence 4, Application US/10136639
 ; Publication No. US20030072761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LeBowitz, Jonathan
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS
 THE BLOOD BRAIN
 ; TITLE OF INVENTION: BARRIER
 ; FILE REFERENCE: SYM-008
 ; CURRENT APPLICATION NUMBER: US/10/136,639
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: US 60/329,650
 ; PRIOR FILING DATE: 2001-10-16
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 7260
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-136-639-4

Query Match 63.9%; Score 334.4; DB 15; Length 7260;
 Best Local Similarity 84.6%; Pred. No. 9e-99;
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	311	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	370
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	371	AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	430
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	431	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Db	491	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC	550
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	551	ATGCCCAAGACCCAG-----	565
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	566	-----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA	618
Qy	361	CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG	420
Db	619	CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG	678
Qy	421	CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT	478

Db 679 CTCTGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy 479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
 || ||||| ||| |||||||||||||||||||||

Db 739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784

RESULT 11

US-10-207-655-54

; Sequence 54, Application US/10207655
 ; Publication No. US20030118592A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Hayden-Ledbetter, Martha S.
 ; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
 ; FILE REFERENCE: 390069.401C1
 ; CURRENT APPLICATION NUMBER: US/10/207,655
 ; CURRENT FILING DATE: 2002-07-25
 ; NUMBER OF SEQ ID NOS: 426
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 54
 ; LENGTH: 725
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-207-655-54

Query Match 63.6%; Score 332.8; DB 15; Length 725;
 Best Local Similarity 84.4%; Pred. No. 9.2e-99;
 Matches 444; Conservative 0; Mismatches 27; Indels 55; Gaps 4;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 ||||||||||||||||| |||||||||||||||||||

Db 156 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 215

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
 ||||||||||||||||| ||||||||||||||||| ||||||||||||||||| |||||

Db 216 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 275

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 ||||| ||||||||||||||||||||||||||||| |||||||||||||||||

Db 276 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 335

Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
 || ||||||||||||| || ||| ||||| ||||| |||||||||||||||||||||

Db 336 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 395

Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 ||||||||| |||

Db 396 ATGCCCAAGACCCAG----- 410

Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 ||||||||||||||||||| |||||||||||||||||||

Db 411 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 463

Qy 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
 ||||||||||||||||| ||||||||||||| ||||| ||||||||||||| |||||

Db 464 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 523

```

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
          ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db      524 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 583

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
          || ||||| ||| ||||| ||||| ||||| ||||| |||||
Db      584 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 629

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RESULT 12

US-10-251-661-7

```

; Sequence 7, Application US/10251661
; Publication No. US20030166555A1
; GENERAL INFORMATION:
; APPLICANT: Alberini, Cristina M.
; APPLICANT: Bear, Mark F.
; TITLE OF INVENTION: Methods and Compositions for Regulating
; TITLE OF INVENTION: Memory Consolidation
; FILE REFERENCE: 3499.1001-003
; CURRENT APPLICATION NUMBER: US/10/251,661
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/193,614
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10661
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)...(564)

```

US-10-251-661-7

```

Query Match          52.3%; Score 273.6; DB 13; Length 612;
Best Local Similarity 83.0%; Pred. No. 2.6e-79;
Matches 347; Conservative 0; Mismatches 19; Indels 52; Gaps 1;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      247 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 306

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      307 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 366

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      367 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 426

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
          || ||||| ||||| || ||| ||||| ||||| ||||| |||||
Db      427 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 486

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```

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        |||||
Db      487 ATGCCCAAGACCCAG----- 501

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        |||||
Db      502 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 554

Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTT 418
        |||||
Db      555 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTT 612

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RESULT 13

US-09-852-261-11

; Sequence 11, Application US/09852261

; Patent No. US20020083477A1

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; APPLICANT: TERENCE, GIORGIO

; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE

; FILE REFERENCE: 117-351

; CURRENT APPLICATION NUMBER: US/09/852,261

; CURRENT FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: GB 0011278.9

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 487

; TYPE: DNA

; ORGANISM: Rattus sp.

US-09-852-261-11

Query Match 50.1%; Score 262; DB 9; Length 487;

Best Local Similarity 74.7%; Pred. No. 1.5e-75;

Matches 396; Conservative 0; Mismatches 75; Indels 59; Gaps 3;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||||
Db      1 GGACAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        |||||
Db      61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTTCGGAGGGCACACAG 120

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        ||
Db      121 ACGGGCATTGTGGATGAGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
        |||||
Db      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        |||||
Db      241 ATGCCCAAGACTCAG----- 255

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